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Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=7; day=7; hr=13; min=47; sec=16; ms=579;]

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Application No: 10582304 Version No: 2.0

Input Set:

Output Set:

Started: 2009-07-06 12:46:32.719
Finished: 2009-07-06 12:46:34.629
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 910 ms
Total Warnings: 15
Total Errors: 0
No. of SeqIDs Defined: 29
Actual SeqID Count: 29

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)

Thr Asp Tyr Asn Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp			
80	85	90	
aaa tcc tcc agc aca gcc tac att ttg ctc agc agc ctg acc tct gag			337
Lys Ser Ser Ser Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu			
95	100	105	
gac tct gcg atg tat ttc tgt gta agg agt gac gac ttt gac tac tgg			385
Asp Ser Ala Met Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp			
110	115	120	
ggc cag ggc acc act ctc aca gtc tcc tca ggt gga ggc ggt tca ggc			433
Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly			
125	130	135	140
gga ggt ggc tct ggc ggt ggc gga agc caa att gtt ctc acc cag tcg			481
Gly Gly Ser Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser			
145	150	155	
cca gca atc atg tct gca tct cca ggg gag aag gtc acc ata acc tgc			529
Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys			
160	165	170	
agt gcc agc tca agt gta agt tac atg cac tgg ttc cag cag aag cca			577
Ser Ala Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro			
175	180	185	
ggc act ttt ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct			625
Gly Thr Phe Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser			
190	195	200	
gga gtc cct act cgc ttc agt ggc agt gga tct ggg acc tct tac tct			673
Gly Val Pro Thr Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser			
205	210	215	220
ctc aca atc agc cga atg gag gct gaa gat gct gcc act tat tac tgc			721
Leu Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys			
225	230	235	
cag caa agg acg agt tat cca ccc acg ttc ggc tcg ggg aca aag ttg			769
Gln Gln Arg Thr Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu			
240	245	250	
gag ata aaa gga ggt ggt ggc agt ggt ggc ggc gga tcc ggt ggc ggt			817
Glu Ile Lys Gly Gly Ser Gly Gly Ser Gly Gly Ser Gly Gly Gly			
255	260	265	
ggc tca cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag cct			865
Gly Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro			
270	275	280	
ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc aca			913
Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr			
285	290	295	300
gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt gaa			961
Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu			

305	310	315	
tgg att gga tgg att ttt cct gga gat gat act act gat tac aat gag Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu 320	325	330	1009
aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc aca Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr 335	340	345	1057
gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg tat Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr 350	355	360	1105
ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc act Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr 365	370	375	1153
ctc aca gtc tcc tca ggt gga ggc ggt tca ggc gga ggt ggc tct ggc Leu Thr Val Ser Ser Gly Gly Ser Gly Gly Gly Ser Gly 385	390	395	1201
ggt ggc gga agc caa att gtt ctc acc cag tcg cca gca atc atg tct Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser 400	405	410	1249
gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc tca agt Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser 415	420	425	1297
gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt ccc aaa Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys 430	435	440	1345
ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct act cgc Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg 445	450	455	1393
ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc agc cga Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg 465	470	475	1441
atg gag gct gaa gat gct gcc act tat tac tgc cag caa agg acg agt Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser 480	485	490	1489
tat cca ccc acg ttc ggc tcg ggg aca aag ttg gag ata aaa gac tac Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr 495	500	505	1537
aag gat gac gac gat aag tga taa gcggccgcaa t Lys Asp Asp Asp Asp Lys 510			1572

<210> 2
<211> 514

<212> PRT

<213> Mus musculus

<400> 2

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
1 5 10 15

Val His Cys Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
65 70 75 80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
100 105 110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Gly Gly Gly Ser
130 135 140

Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met
145 150 155 160

Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser
165 170 175

Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro
180 185 190

Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr
195 200 205

Arg Phe Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
210 215 220

Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr
225 230 235 240

Ser Tyr Pro Pro Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Gly
245 250 255

Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser Gln Val
260 265 270

Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala Ser Val
275 280 285

Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Phe Ile
290 295 300

His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Trp
305 310 315 320

Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg Gly
325 330 335

Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Ile Leu
340 345 350

Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met Tyr Phe Cys Val Arg
355 360 365

Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser
370 375 380

Ser Gly Gly Gly Ser Gly Gly Ser Gly Gly Gly Ser
385 390 395 400

Gln Ile Val Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly
405 410 415

Glu Lys Val Thr Ile Thr Cys Ser Ala Ser Ser Ser Val Ser Tyr Met
420 425 430

His Trp Phe Gln Gln Lys Pro Gly Thr Phe Pro Lys Leu Trp Ile Tyr
435 440 445

Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Thr Arg Phe Ser Gly Ser
450 455 460

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
465 470 475 480

Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Thr Ser Tyr Pro Pro Thr
485 490 495

Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp Asp Asp
500 505 510

Asp Lys

<210> 3
<211> 5
<212> PRT
<213> Mus musculus

<400> 3
Asp Tyr Phe Ile His
1 5

<210> 4
<211> 17
<212> PRT
<213> Mus musculus

<400> 4
Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn Glu Lys Phe Arg
1 5 10 15

Gly

<210> 5
<211> 6
<212> PRT
<213> Mus musculus

<400> 5
Ser Asp Asp Phe Asp Tyr
1 5

<210> 6
<211> 10
<212> PRT
<213> Mus musculus

<400> 6
Ser Ala Ser Ser Ser Val Ser Tyr Met His
1 5 10

<210> 7
<211> 7
<212> PRT
<213> Mus musculus

<400> 7
Ser Thr Ser Asn Leu Ala Ser
1 5

<210> 8
<211> 9
<212> PRT
<213> Mus musculus

<400> 8

Gln Gln Arg Thr Ser Tyr Pro Pro Thr
1 5

<210> 9
<211> 402
<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(402)

<400> 9

atg cga tgg agc tgg atc ttt ctc ttc ctc ctg tca ata act gca ggt 48
Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
1 5 10 15

gtc cat tgc cag gtc cag ttg cag cag tct gga cct gag ctg gtg aag 96
Val His Cys Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

cct ggg gct tca gtg aag atg tct tgt aag gct tct ggc tac acc ttc 144
Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

aca gac tac ttt ata cac tgg gtg aaa cag agg cct gga cag gga ctt 192
Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu
50 55 60

gaa tgg att gga tgg att ttt cct gga gat gat act act gat tac aat 240
Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn
65 70 75 80

gag aag ttc agg ggc aag acc aca ctg act gca gac aaa tcc tcc agc 288
Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser
85 90 95

aca gcc tac att ttg ctc agc agc ctg acc tct gag gac tct gcg atg 336
Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met
100 105 110

tat ttc tgt gta agg agt gac gac ttt gac tac tgg ggc cag ggc acc 384
Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr
115 120 125

act ctc aca gtc tcc tca 402
Thr Leu Thr Val Ser Ser
130

<210> 10

<211> 134

<212> PRT

<213> Mus musculus

<400> 10

Met Arg Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Ile Thr Ala Gly
1 5 10 15

Val His Cys Gln Val Gln Leu Gln Ser Gly Pro Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe

35

40

45

Thr Asp Tyr Phe Ile His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu

50

55

60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Asp Thr Thr Asp Tyr Asn

65

70

75

80

Glu Lys Phe Arg Gly Lys Thr Thr Leu Thr Ala Asp Lys Ser Ser Ser

85

90

95

Thr Ala Tyr Ile Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Met

100

105

110

Tyr Phe Cys Val Arg Ser Asp Asp Phe Asp Tyr Trp Gly Gln Gly Thr

115

120

125

Thr Leu Thr Val Ser Ser

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<211> 384

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<220>

<221> CDS

<222> (1)..(384)

<400> 11

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Met His Phe Gln Val Gln Ile Phe Ser Phe Leu Leu Ile Ser Ala Ser
1 5 10 15

48

gtc atc atg tcc aga gga caa att gtt ctc acc cag tcg cca gca atc
Val Ile Met Ser Arg Gly Gln Ile Val Leu Thr Gln Ser Pro Ala Ile
20 25 30

96

atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc
Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
35 40 45

144

tca agt gta agt tac atg cac tgg ttc cag cag aag cca ggc act ttt
Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Phe
50 55 60

192

ccc aaa ctc tgg att tat agc aca tcc aac ctg gct tct gga gtc cct
Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
65 70 75 80

240

act cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc
Thr Arg Phe Ser Gly

288